

RAW SEQUENCE LISTING

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Application Serial Number: 10/531, 777
Source: PCT
Date Processed by STIC: 02/09/2006

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DATE: 02/09/2006

PATENT APPLICATION: US/10/531,777

TIME: 15:02:01

Input Set : A:\PRD0054-US.Sequence Listing.txt

Output Set: N:\CRF4\02092006\J531777.raw

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3 <110> APPLICANT: Barbier, Ann Johanna
4     Wilson, Sandy J.
5     Mazur, Curt
7 <120> TITLE OF INVENTION: Assay for Determining the Activity of Fatty Acid Amide
Hydrolase
9 <130> FILE REFERENCE: PRI0002
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/531,777
C--> 11 <141> CURRENT FILING DATE: 2005-04-19
11 <160> NUMBER OF SEQ ID NOS: 8
13 <170> SOFTWARE: PatentIn version 3.1
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 2300
17 <212> TYPE: DNA
18 <213> ORGANISM: Sus scrofa
20 <400> SEQUENCE: 1
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23 cgggggttgcc ctggcctgct gcttgggtggc agcggccttg gccctgcgtt ggtccagtcg      120
25 ccggatggcg cggggcgcg cggcccgggc gcgacagagg cagcaagcgg ccctggagac      180
27 catggacaag gcggcgcgagc gcttcgggct ccagaacccc gatctggact cggagatgct      240
29 gctggccctg ccactgcctc agctggtaca gaaggtaoga agtggggagc tgtctccaga      300
31 ggctgtgctc ttttcctacc tgcaaaaggc ctgggaagtg aacagagggg ccaactgcgt      360
33 gaccacctac ctggcagact gtgaggetca gctgtgccag gcgcccgggc agggcctgct      420
35 ctacgggtgtc ccgcgcagcc tcaaggagtg cttcagctgc aagggccatg actccacgct      480
37 gggcttgagc cggaaccagg ggacaccagc agaatgtgac tgcgtggtgg tgcaggtgct      540
39 gaaactgcag ggtgctgtgc ctttcgtgca caccaacgtc cccagtgcca tgttcagcta      600
41 tgactgcagt aacccccctc ttggccagac cagcaaccca tggatgtcgt ccaagagccc      660
43 gggcggctcc tcgggaggtg agggggccct cattgctgct ggaggctccc cactgggctt      720
45 aggcaccgac atcgggggca gcatccgctt tccctccgcc ttctgtggca tctgcggcat      780
47 caaaccacag gggaaccgca tcagcaagag tggctctgaag ggctctgtct atggacaggt      840
49 agcagtgcag ctctcagtg gcccctatgg gcgggacgtg gagagcctgg ccctgtgct      900
51 gcgtgcgctg ctgtgcgaag acatgttccg cctggacccc acggtgcctc ccctgccctt      960
53 caacgaggag gtctacgcaa gctctcgccc cctgcgtgtc gggattatg agaccgacaa      1020
55 ctacaccatg ccacgcggc ccatgaggcg ggcctgctg gagaccaagc ggagccttga      1080
57 ggctgcgggc cacacgctga ttcccttcc tccggccaac atacccacg ctctggaggc      1140
59 cctgtcaacg ggcgggctct tcagtgatgg tgggaagagg ttgctacaga acttcgaagg      1200
61 cgattacgtg gactcctgct taggggacct gatctcaatt ctgaggctgc ccaaattggct      1260
63 taaaggactg ctggctttca tgctgaggcc tctgctccca aggttggcag gctttctcag      1320
65 cagcctgagg cctcggtcgg ctggaaagct ctgggaactg cagcacgaga ttgagatgta      1380
67 ccgtcactcc gtgattgccc agtggcgagc gctggacctg gatgtggtgc taacccccat      1440
69 gctgagccct gccctagact tgaatgcccc aggcaaggcc acaggggccc tcagctacac      1500
71 gctgctctac aactgcctgg acttccccgc gggggtggtg cctgtcacca cggtgactgc      1560
73 cgaggacgag gcccatgatg agcattacaa gggctacttt ggggacattt gggacaaggt      1620
75 ggtgcagaag gccatgaaga ggagcgtggg gctgcctgtg gccgtgcagt gtgtggctct      1680
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79 tgggcgccag ccctcctgac cgctgcccgc cgggcccccc aggacctgag acccactgga 1800
81 tccgcgcccc gcgagtcag gacacaactg ccaccgtgca agaaaatgtt caacctcagg 1860
83 cagaggcttc cgggtctctc cccctcgccc ctgccagaag cccagaacca ctgagtctgg 1920
85 accttgctct tcccggtggtc cctgctctgc cctgaccccg ccaatgtggc agctagtggg 1980
87 tatgacatgg caaaggcccc ccaaccgtca aaaaccgggt cctgggtctcc atactttctg 2040
89 gcagtcggtt ttagggcagt ggggggttga gacctgacct tctggaaccc gactccagcc 2100
91 atgtccgtct cgtgctgcag aagcttctct ggtcctcgtc actcacgggc agacaccggc 2160
93 ttctccgagt gggccttgca gccaggact tcaccccgcc gccccagcc taagccctac 2220
95 tttgcgaggg attgtcttct ctctgcctct ctgctgaggg tgccctttct gctcctctac 2280
97 cattaaatcc tttgaggccc                                     2300

100 <210> SEQ ID NO: 2
101 <211> LENGTH: 579
102 <212> TYPE: PRT
103 <213> ORGANISM: Sus scrofa
105 <400> SEQUENCE: 2
107 Met Val Gln Glu Leu Trp Ala Ala Phe Ser Gly Pro Ser Gly Val
108 1 5 10 15
111 Ala Leu Ala Cys Cys Leu Val Ala Ala Ala Leu Ala Leu Arg Trp Ser
112 20 25 30
115 Ser Arg Arg Met Ala Arg Gly Ala Ala Ala Arg Ala Arg Gln Arg Gln
116 35 40 45
119 Gln Ala Ala Leu Glu Thr Met Asp Lys Ala Ala Gln Arg Phe Arg Leu
120 50 55 60
123 Gln Asn Pro Asp Leu Asp Ser Glu Met Leu Leu Ala Leu Pro Leu Pro
124 65 70 75 80
127 Gln Leu Val Gln Lys Val Arg Ser Gly Glu Leu Ser Pro Glu Ala Val
128 85 90 95
131 Leu Phe Ser Tyr Leu Gln Lys Ala Trp Glu Val Asn Arg Gly Thr Asn
132 100 105 110
135 Cys Val Thr Tyr Leu Ala Asp Cys Glu Ala Gln Leu Cys Gln Ala
136 115 120 125
139 Pro Gly Gln Gly Leu Leu Tyr Gly Val Pro Val Ser Leu Lys Glu Cys
140 130 135 140
143 Phe Ser Cys Lys Gly His Asp Ser Thr Leu Gly Leu Ser Arg Asn Gln
144 145 150 155 160
147 Gly Thr Pro Ala Glu Cys Asp Cys Val Val Val Gln Val Leu Lys Leu
148 165 170 175
151 Gln Gly Ala Val Pro Phe Val His Thr Asn Val Pro Gln Ser Met Phe
152 180 185 190
155 Ser Tyr Asp Cys Ser Asn Pro Leu Phe Gly Gln Thr Thr Asn Pro Trp
156 195 200 205
159 Met Ser Ser Lys Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu
160 210 215 220
163 Ile Ala Ala Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly
164 225 230 235 240
167 Ser Ile Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Ile Lys Pro
168 245 250 255
171 Thr Gly Asn Arg Ile Ser Lys Ser Gly Leu Lys Gly Ser Val Tyr Gly
172 260 265 270

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175 Gln Val Ala Val Gln Leu Ser Val Gly Pro Met Ala Arg Asp Val Glu
176      275      280      285
179 Ser Leu Ala Leu Cys Leu Arg Ala Leu Leu Cys Glu Asp Met Phe Arg
180      290      295      300
183 Leu Asp Pro Thr Val Pro Pro Leu Pro Phe Asn Glu Glu Val Tyr Ala
184 305      310      315      320
187 Ser Ser Arg Pro Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr
188      325      330      335
191 Met Pro Thr Pro Ala Met Arg Arg Ala Leu Leu Glu Thr Lys Arg Ser
192      340      345      350
195 Leu Glu Ala Ala Gly His Thr Leu Ile Pro Phe Leu Pro Ala Asn Ile
196      355      360      365
199 Pro His Ala Leu Glu Ala Leu Ser Thr Gly Gly Leu Phe Ser Asp Gly
200      370      375      380
203 Gly Lys Arg Leu Leu Gln Asn Phe Glu Gly Asp Tyr Val Asp Ser Cys
204 385      390      395      400
207 Leu Gly Asp Leu Ile Ser Ile Leu Arg Leu Pro Lys Trp Leu Lys Gly
208      405      410      415
211 Leu Leu Ala Phe Met Leu Arg Pro Leu Leu Pro Arg Leu Ala Gly Phe
212      420      425      430
215 Leu Ser Ser Leu Arg Pro Arg Ser Ala Gly Lys Leu Trp Glu Leu Gln
216      435      440      445
219 His Glu Ile Glu Met Tyr Arg His Ser Val Ile Ala Gln Trp Arg Ala
220      450      455      460
223 Leu Asp Leu Asp Val Val Leu Thr Pro Met Leu Ser Pro Ala Leu Asp
224 465      470      475      480
227 Leu Asn Ala Pro Gly Lys Ala Thr Gly Ala Val Ser Tyr Thr Leu Leu
228      485      490      495
231 Tyr Asn Cys Leu Asp Phe Pro Ala Gly Val Val Pro Val Thr Thr Val
232      500      505      510
235 Thr Ala Glu Asp Glu Ala Gln Met Glu His Tyr Lys Gly Tyr Phe Gly
236      515      520      525
239 Asp Ile Trp Asp Lys Val Val Gln Lys Ala Met Lys Arg Ser Val Gly
240      530      535      540
243 Leu Pro Val Ala Val Gln Cys Val Ala Leu Pro Trp Gln Glu Glu Leu
244 545      550      555      560
247 Cys Leu Arg Phe Met Arg Glu Val Glu Arg Leu Met Ala Pro Gly Arg
248      565      570      575
251 Gln Pro Ser
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 1740
257 <212> TYPE: DNA
258 <213> ORGANISM: Mouse
260 <400> SEQUENCE: 3

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261 atggtgctga gcgaagtgtg gaccgcgctg tctggactct ccgggggttg cctagcctgc      60
263 agcttgctgt cggcggcggt ggtcctgcga tggaccagga gccagaccgc ccggggcgcg      120
265 gtgaccaggg cgcgcgagaa gcagcgagcc ggcctggaga ccatggacaa ggcggtgcag      180
267 cgcttcgggc tgcagaatcc tgacctgat tcaaggcct tgctggctct gccctgctc      240
269 caactggtac agaagttaca gagtggggaa ctgtccccag aagctgtgct ctttacctac      300

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271 ctgggaaagg cctgggaagt gaacaaaggg accaactgtg tgacctccta tctgactgac 360
273 tgtgagactc agctgtccca ggccccacgg cagggcctgc tctatggcgt ccccgtagac 420
275 ctcaaggaat gcttcagcta caagggccat gcttcacacac tgggcttaag tttgaacgag 480
277 ggtgtgacat cggagagtga ctgtgtggtg gtgcaggtag tgaagctgca gggagctgtg 540
279 ccctttgtgc acaccaacgt cccccagtc atgctaagct atgactgcag taacccccctc 600
281 tttggccaga ccatgaaccc gtggaagccc tccaagagtc caggagggtt ctcagggggt 660
283 gagggggctc tcattggatc tggaggctcc cctctgggtt taggcactga catcggcggc 720
285 agcatccggt tcccttctgc cttctgtggc atctgtggcc tcaagcctac tgggaaccgc 780
287 ctcagcaaga gtggcctgaa gagctgtgtt tatggacaga cagcagtgcg gctttctgtt 840
289 ggccccatgg caggggatgt ggatagcctg gcattgtgca tgaaagccct actttgtgag 900
291 gatttgttcc gcttggactc caccatcccc cccttgccct tcagggagga gatctacaga 960
293 agttctcgac cccttcgtgt gggatactat gaaactgaca actacaccat gccactcca 1020
295 gccatgagga gggctgtgat ggagaccaag cagagtctcg aggtgctgg ccacacgctg 1080
297 gtcccccttct taccaaaca cataccttat gccctggagg tctgtcggc aggtgggctg 1140
299 ttcagtgatg gtggctgctc ttttctccaa aacttcaaag gcgactttgt ggatccctgc 1200
301 ttgggggacc tggcttagt gctgaagctg ccaggtggt ttaaaaaact gctgagcttc 1260
303 ctgctgaagc ctctgttcc tcggctggca gcctttctca acagtatgtg tctcgggtca 1320
305 gccgaaaagc tgtgggaact gcagcatgag attgagatgt atcgccagtc cgtcattgcc 1380
307 cagtggaagg caatgaactt ggacgtggtg ctaacccccca tgctgggtcc tgctctggat 1440
309 ttgaacgcac cgggcagagc cacaggggct atcagctaca ctgttctcta taactgcctg 1500
311 gacttccctg cgggggtggt gcctgtcacc actgtgaccg ctgaggacga tgcccagatg 1560
313 gaacactaca aaggctactt tggggatatg tgggacaaca ttctgaagaa gggcatgaaa 1620
315 aagggtatag gcctgcctgt ggctgtgcag tgcgtggctc tgccctggca ggaagagctg 1680
317 tgtctgcggt tcatgcggga ggtggaacgg ctgatgaccc ctgaaaagcg gccatcttga 1740

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320 <210> SEQ ID NO: 4

321 <211> LENGTH: 579

322 <212> TYPE: PRT

323 <213> ORGANISM: Mouse

325 <400> SEQUENCE: 4

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327 Met Val Leu Ser Glu Val Trp Thr Ala Leu Ser Gly Leu Ser Gly Val
328 1 5 10 15
331 Cys Leu Ala Cys Ser Leu Leu Ser Ala Ala Val Val Leu Arg Trp Thr
332 20 25 30
335 Arg Ser Gln Thr Ala Arg Gly Ala Val Thr Arg Ala Arg Gln Lys Gln
336 35 40 45
339 Arg Ala Gly Leu Glu Thr Met Asp Lys Ala Val Gln Arg Phe Arg Leu
340 50 55 60
343 Gln Asn Pro Asp Leu Asp Ser Glu Ala Leu Leu Ala Leu Pro Leu Leu
344 65 70 75 80
347 Gln Leu Val Gln Lys Leu Gln Ser Gly Glu Leu Ser Pro Glu Ala Val
348 85 90 95
351 Leu Phe Thr Tyr Leu Gly Lys Ala Trp Glu Val Asn Lys Gly Thr Asn
352 100 105 110
355 Cys Val Thr Ser Tyr Leu Thr Asp Cys Glu Thr Gln Leu Ser Gln Ala
356 115 120 125
359 Pro Arg Gln Gly Leu Leu Tyr Gly Val Pro Val Ser Leu Lys Glu Cys
360 130 135 140
363 Phe Ser Tyr Lys Gly His Ala Ser Thr Leu Gly Leu Ser Leu Asn Glu
364 145 150 155 160

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367 Gly Val Thr Ser Glu Ser Asp Cys Val Val Val Gln Val Leu Lys Leu
368          165          170          175
371 Gln Gly Ala Val Pro Phe Val His Thr Asn Val Pro Gln Ser Met Leu
372          180          185          190
375 Ser Tyr Asp Cys Ser Asn Pro Leu Phe Gly Gln Thr Met Asn Pro Trp
376          195          200          205
379 Lys Pro Ser Lys Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu
380          210          215          220
383 Ile Gly Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly
384 225          230          235          240
387 Ser Ile Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro
388          245          250          255
391 Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys Ser Cys Val Tyr Gly
392          260          265          270
395 Gln Thr Ala Val Gln Leu Ser Val Gly Pro Met Ala Arg Asp Val Asp
396          275          280          285
399 Ser Leu Ala Leu Cys Met Lys Ala Leu Leu Cys Glu Asp Leu Phe Arg
400          290          295          300
403 Leu Asp Ser Thr Ile Pro Pro Leu Pro Phe Arg Glu Glu Ile Tyr Arg
404 305          310          315          320
407 Ser Ser Arg Pro Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr
408          325          330          335
411 Met Pro Thr Pro Ala Met Arg Arg Ala Val Met Glu Thr Lys Gln Ser
412          340          345          350
415 Leu Glu Ala Ala Gly His Thr Leu Val Pro Phe Leu Pro Asn Asn Ile
416          355          360          365
419 Pro Tyr Ala Leu Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly
420          370          375          380
423 Gly Cys Ser Phe Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys
424 385          390          395          400
427 Leu Gly Asp Leu Val Leu Val Leu Lys Leu Pro Arg Trp Phe Lys Lys
428          405          410          415
431 Leu Leu Ser Phe Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe
432          420          425          430
435 Leu Asn Ser Met Cys Pro Arg Ser Ala Glu Lys Leu Trp Glu Leu Gln
436          435          440          445
439 His Glu Ile Glu Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala
440          450          455          460
443 Met Asn Leu Asp Val Val Leu Thr Pro Met Leu Gly Pro Ala Leu Asp
444 465          470          475          480
447 Leu Asn Ala Pro Gly Arg Ala Thr Gly Ala Ile Ser Tyr Thr Val Leu
448          485          490          495
451 Tyr Asn Cys Leu Asp Phe Pro Ala Gly Val Val Pro Val Thr Thr Val
452          500          505          510
455 Thr Ala Glu Asp Asp Ala Gln Met Glu His Tyr Lys Gly Tyr Phe Gly
456          515          520          525
459 Asp Met Trp Asp Asn Ile Leu Lys Lys Gly Met Lys Lys Gly Ile Gly
460          530          535          540
463 Leu Pro Val Ala Val Gln Cys Val Ala Leu Pro Trp Gln Glu Glu Leu

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date